claim for replacement of PCT

13.-A method for the screening of antimycotic substances wherein an essential gene from mycetes or a functionally similar mycete gene, or the corresponding encoded protein, is used as target and wherein the essential gene is selected from the group consisting in YML114c, YLR186w, YLR215c, YLR222c, YLR243w, YLR272c, YLR275w, YLR276c, YLR317w, YLR359w, YLR373c, YLR424w, YLR437c, YLR440c, YML023c, YML049c, YML077w, YML093w, YML127w, YMR032w, YMR093w, YMR131c, YMR185w, YMR212c, YMR213w, YMR218c, YMR281w, YMR288w, YMR290c, YMR211w, YMR049c, YMR134w, YDR196c, YDR299w, YDR365c, YDR396w, YDR407c, YDR416w, YDR449c, YDR472w, YDR499w, YDR141c, YDR324c, YDR325w, YDR398w, YDR246w, YDR236c, YDR361c, YDR367w, YDR339c, YDR413c, YDR429c, YDR468c, YDR489w, YDR527w, YDR288w, YDR201w, YDR434w, YDR181c, YDR531w, YPL126w, YPL093w, YPL063w, YPL024w, YPL020c, YPL012w, YPL007c, YPL233w, YPL146c, YIL091c, YIL083c, YIL019w, YIL109c, YIL104c, YFL024c, YFR003c, YFR027w, YFR042w, YIR010w, YIR015w, YPR048w, YPR072w, YPR082c, YPR085c, YPR105c, YPR112c, YPR137w, YPR143w, YPR144c and YPR169w.

14.-The method of claim 13 wherein mycete cells which express the essential gene, or a functionally similar mycete gene, to a different level are incubated with the substance to be tested and the growth inhibiting effect of the substance is determined.

15.-The method of claim 13 wherein said target gene or the corresponding target encoded protein is contacted in vitro with the substance to be tested and the effect of the substance on the target is determined.

16.-The method according to claim 13 wherein the screened substances partially or totally inhibit the functional expression of the essential genes or the functional activity of the encoded proteins.

17.-The method according to claim 14 wherein the screened substances partially or totally inhibit the functional expression of the essential genes or the functional activity of the encoded proteins.

18.-The method according to claim 15 wherein the screened substances partially or totally inhibit the functional expression of the essential genes or the functional activity of the encoded proteins.

19.-The method according to claim 13 wherein the mycete species are selected from the group comprising Basidiomycetes, Ascomycetes and Hyphomycetes.

20.- The method according to claim 13, wherein said functionally similar genes are essential genes from Candida Spp, or Aspergillus Spp.

21.- The method according to claim 20, wherein said functionally similar genes are essential genes from Candida albicans, or Aspergillus fumigatus.

22.- The method according to claim 13 wherein the functionally similar genes are identified by:

a) providing a S.cerevisiae mutant strain in which the gene of S.cerevisiae to be investigated is either integrative or extrachromosomal under the control of a regulated promoter,

b) culturing said mutant strain under growth conditions in which the regulated promoter is active,

c) transforming the mutant strain with cDNA or genomic DNA that has been prepared from the mycete-species to investigate and that has been integrated into an appropriate vector,

d) altering the culture condition, so that the regulated promoter is switched off and only S.cerevisiae cells which contain a functionally similar gene can survive,

e) isolating and analyzing the cDNA or genomic DNA.

23.- The method according to claim 22 wherein the functionally similar gene has a sequence identity, at the nucleotide level, with the corresponding S.cerevisiae essential gene of at least 50%, preferably of at least 60%, and most preferably of at least 70%.

24.- The method according to claim 22 wherein the functionally similar gene encodes a protein having a sequence identity, at the amino-acid level, with the corresponding S.cerevisiae essential gene encoded protein of at least 40%, preferably of at least 50%, more preferably of at least 60% and most preferably of at least 70%.

25.- The method according to claim 13 wherein said mycete cells are haploid S.cerevisiae cells.

26.- The method according to claim 22 wherein said mycete cells are haploid S.cerevisiae cells.

27.- The method according to claim 13 wherein the essential genes of S.cerevisiae are identified by integration through homologous recombination of a selection marker at the locus of the gene to be studied.

28.- The method according to claim 25 wherein the essential genes of S.cerevisiae are identified by integration through homologous recombination of a selection marker at the locus of the gene to be studied.